

## SEQUENCE LISTING

<110> Giese, Klaus  
Xin, Hong

<120> METASTATIC BREAST AND COLON CANCER REGULATED GENES

<130> 1451.002 / 210030.447

<140> US 09/215,450

<141> 1998-12-17

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2429

<212> DNA

<213> human

<400> 1

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<210> 2

<211> 486

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(486)

<223> n = A,T,C or G

<400> 2

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<210> 3

<211> 397

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(397)

<223> n = A,T,C or G

<400> 3

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ttctagtggg aaagataaat aacatgctca ggaaatttta gcagagagat agaaactatg 240
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<210> 4

<211> 376

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 4

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tgtaagaaca	ccaatcttat	tggatgctat	aggcctccac	ccttatgacg	tcattaaact	360
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&lt;210&gt; 5

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 2730

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 6

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cagccaatga	ccagcagttg	gtatgaagaa	cctttgacat	tttgtaaaag	gccatttctt	2640
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<210> 7

<211> 218

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(218)

<223> n = A,T,C or G

<400> 7

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ccgagacaat	ataaatgtac	aatggatacc	cgatgcaaac	aatgtattgt	ggttaactag	180
gtgtnatccc	ncccattgtg	ntantaaggg	cngntgtc			218

<210> 8

<211> 426

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(426)

<223> n = A,T,C or G

<400> 8

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attaaa 426

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<210> 9
<211> 480
<212> DNA
<213> human

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<220>
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<222> (1)...(480)
<223> n = A,T,C or G

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gggggcnatt nncataccnt ggaatttaac cccnttctna ctgttcttnt ttgaatnnat 420
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<210> 10
<211> 402
<212> DNA
<213> human

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<220>
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<222> (1)...(402)
<223> n = A,T,C or G

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<400> 10
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<210> 11
<211> 575
<212> DNA
<213> human

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<220>
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<222> (1)...(575)

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<223> n = A,T,C or G

<400> 11

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ccaaaacagt	gggtactgt	atcatcccta	tatgcttggc	agttatttgc	aatcgccacc	360
aggcatttgt	caaggcttct	aatcagatca	gcagactaca	actgattgac	acgtnaaatc	420
agtcaccgtt	ttttccctac	nattacaaaa	ctgccagtcc	tatatggagt	ctgatcacia	480
gactgcagtt	tcttcacaga	tctcaggaag	ttgtcgtggg	gcanaagctt	tttaaaaaca	540
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<210> 12

<211> 442

<212> DNA

<213> human

<400> 12

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ttgggtgtaa	ataagcagac	agaaaatcta	agaatcaac	agactgagaa	tctacttaaa	180
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cattatgtat	atagtacact	taccaggaat	cgagtttagac	aaccagaaaa	gcccawagca	300
akatttgctg	aaawgttcta	aaagcatgcr	caatgtgact	cataacttgg	aggaggatga	360
ggagggaagt	accaagaaga	aactctccaa	gtggcactac	taccaaataca	gtttccattg	420
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<210> 13

<211> 332

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 13

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ggagtctgga	aggttttctc	tagagtcttg	gaaagtttct	taagtgggcc	ctggtacaag	180
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tggggtcata	atgggtttgt	tttcgtattc	cancggttgt	actcaggcac	cagtttcccc	300
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<210> 14

<211> 970

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1) ... (970)

<223> n = A,T,C or G

<400> 14

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gaaaaaatgt catcgaccct cccatctatg cagcacacat aagaatcctt ccttggtcct	660
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<210> 15

<211> 528

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1) ... (528)

<223> n = A,T,C or G

<400> 15

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ttagcaatct ctatattctt tcaagtaacc aagctgttga ctttcttact acttgcagta	180
gcctgtcccc aactttttcca tccagtgtt aaacctaaaa actccttaac tctgccttga	240
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<211> 518
<212> PRT
<213> human

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Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
35          40          45
Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
50          55          60
Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65          70          75          80
Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
85          90          95
Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100         105         110
Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
115         120         125
Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
130         135         140
Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
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 <213> human

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26

<210> 22  
 <211> 396  
 <212> PRT  
 <213> Homo sapien

<400> 22  
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 Lys Lys Lys Leu Arg Ala Arg Ser Gln Leu Ser Glu Phe Trp Lys Ser  
 35 40 45  
 His Asn Leu Asp Met Ile Gln Phe Thr Glu Ser Cys Ser Met Asp Gln  
 50 55 60  
 Ser Ala Lys Glu Pro Leu Ile Asn Tyr Leu Asp Met Glu Tyr Phe Gly  
 65 70 75 80  
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 Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Val Tyr Cys Thr Ser Pro  
 100 105 110  
 Ala Cys Lys Thr His Ser Arg Phe Gln Pro Ser Gln Ser Ser Thr Tyr  
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 Val Gly Gln Gln Phe Gly Glu Ser Val Thr Glu Pro Gly Gln Thr Phe  
 165 170 175  
 Val Asp Ala Glu Phe Asp Gly Ile Leu Gly Leu Gly Tyr Pro Ser Leu  
 180 185 190  
 Ala Val Gly Gly Val Thr Pro Val Phe Asp Asn Met Met Ala Gln Asn  
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 210 215 220  
 Gly Gly Ala Gly Ser Glu Leu Ile Phe Gly Gly Tyr Asp His Ser His  
 225 230 235 240  
 Phe Ser Gly Ser Leu Asn Trp Val Pro Val Thr Lys Gln Ala Tyr Trp  
 245 250 255  
 Gln Ile Ala Leu Asp Asn Ile Gln Val Gly Gly Thr Val Met Phe Cys  
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 Ser Glu Gly Cys Gln Ala Ile Val Asp Thr Gly Thr Ser Leu Ile Thr  
 275 280 285  
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 Pro Val Asp Gly Glu Tyr Ala Val Glu Cys Ala Asn Leu Asn Val Met  
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<400> 23

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Ser	Ser	Asn	Leu	Trp	Val	Pro	Ser	Val	Tyr	Cys	Ser	Ser	Leu	Ala	Cys
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Thr	Asn	His	Asn	Arg	Phe	Asn	Pro	Glu	Asp	Ser	Ser	Thr	Tyr	Gln	Ser
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145				150						155					160
Gln	Ile	Phe	Gly	Leu	Ser	Glu	Thr	Glu	Pro	Gly	Ser	Phe	Leu	Tyr	Tyr
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 325 330 335  
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 <211> 388  
 <212> PRT  
 <213> Homo sapien

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 35 40 45  
 Asp Pro Ala Trp Lys Tyr Arg Phe Gly Asp Leu Ser Val Thr Tyr Glu  
 50 55 60  
 Pro Met Ala Tyr Met Asp Ala Ala Tyr Phe Gly Glu Ile Ser Ile Gly  
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 Thr Pro Pro Gln Asn Phe Leu Val Leu Phe Asp Thr Gly Ser Ser Asn  
 85 90 95  
 Leu Trp Val Pro Ser Val Tyr Cys Gln Ser Gln Ala Cys Thr Ser His  
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 Ser Arg Phe Asn Pro Ser Glu Ser Ser Thr Tyr Ser Thr Asn Gly Gln  
 115 120 125  
 Thr Phe Ser Leu Gln Tyr Gly Ser Gly Ser Leu Thr Gly Phe Phe Gly  
 130 135 140  
 Tyr Asp Thr Leu Thr Val Gln Ser Ile Gln Val Pro Asn Gln Glu Phe  
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 165 170 175  
 Asp Gly Ile Met Gly Leu Ala Tyr Pro Ala Leu Ser Val Asp Glu Ala  
 180 185 190  
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Gln Phe Leu Val Asn Cys Asn Ser Ile Gln Asn Leu Pro Ser Leu Thr					
305		310		315	
Phe Ile Ile Asn Gly Val Glu Phe Pro Leu Pro Pro Ser Ser Tyr Ile					
325		330		335	
Leu Ser Asn Asn Gly Tyr Cys Thr Val Gly Val Glu Pro Thr Tyr Leu					
340		345		350	
Ser Ser Gln Asn Gly Gln Pro Leu Trp Ile Leu Gly Asp Val Phe Leu					
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<210> 25  
 <211> 412  
 <212> PRT  
 <213> Homo sapien

<400> 25

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35	40	45			
Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro Ala Val Thr Glu					
50	55	60			
Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr					
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Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe					
85	90	95			
Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu					
100	105	110			
Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser					
115	120	125			
Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser					
130	135	140			
Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys					
145	150	155		160	
Gln Ser Ala Ser Ser Ala Ser Ala Leu Gly Gly Val Lys Val Glu Arg					
165	170	175			
Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala					
180	185	190			
Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val					
195	200	205			
Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val					
210	215	220			
Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln					

( )

<400> 26

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Arg	Ile	Phe	Leu	Lys	Arg	Met	Pro	Ser	Ile	Arg	Glu	Ser	Leu	Lys	Glu
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Gln	Thr	Phe	Lys	Val	Val	Phe	Asp	Thr	Gly	Ser	Ser	Asn	Val	Trp	Val
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Leu	Thr	Leu	Arg	Tyr	Ser	Thr	Gly	Thr	Val	Ser	Gly	Phe	Leu	Ser	Gln
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Asp	Ile	Ile	Thr	Val	Gly	Gly	Ile	Thr	Val	Thr	Gln	Met	Phe	Gly	Glu
				165					170					175	
Val	Thr	Glu	Met	Pro	Ala	Leu	Pro	Phe	Met	Leu	Ala	Glu	Phe	Asp	Gly



	180		185		190										
Val	Val	Gly	Met	Gly	Phe	Ile	Glu	Gln	Ala	Ile	Gly	Arg	Val	Thr	Pro
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Ser	Phe	Tyr	Tyr	Asn	Arg	Asp	Ser	Glu	Asn	Ser	Gln	Ser	Leu	Gly	Gly
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His	Tyr	Ile	Asn	Leu	Ile	Lys	Thr	Gly	Val	Trp	Gln	Ile	Gln	Met	Lys
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Gly	Val	Ser	Val	Gly	Ser	Ser	Thr	Leu	Leu	Cys	Glu	Asp	Gly	Cys	Leu
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Ala	Leu	Val	Asp	Thr	Gly	Ala	Ser	Tyr	Ile	Ser	Gly	Ser	Thr	Ser	Ser
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Ile	Glu	Lys	Leu	Met	Glu	Ala	Leu	Gly	Ala	Lys	Lys	Arg	Leu	Phe	Asp
	305					310					315				320
Tyr	Val	Val	Lys	Cys	Asn	Glu	Gly	Pro	Thr	Leu	Pro	Asp	Ile	Ser	Phe
			325						330					335	
His	Leu	Gly	Gly	Lys	Glu	Tyr	Thr	Leu	Thr	Ser	Ala	Asp	Tyr	Val	Phe
		340						345				350			
Gln	Glu	Ser	Tyr	Ser	Ser	Lys	Lys	Leu	Cys	Thr	Leu	Ala	Ile	His	Ala
		355					360					365			
Met	Asp	Ile	Pro	Pro	Pro	Thr	Gly	Pro	Thr	Trp	Ala	Leu	Gly	Ala	Thr
	370					375					380				
Phe	Ile	Arg	Lys	Phe	Tyr	Thr	Glu	Phe	Asp	Arg	Arg	Asn	Asn	Arg	Ile
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Gly	Phe	Ala	Leu	Ala	Arg										
					405										

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ggatgtaacc aagctgtacc cttgagacct ggaaccagag ccacaggccc cttttgtggg	360
tttctctgtg ctctgaatgg gagccagaat tcactaggag gtcatacaacc gatggtcctc	420
acaagcctct tctgaagatg gaaggccttt tgcccgttga ggtagagggg aaggaaatct	480
cctcttttgt acccaatact tatgttgtat tgttgggtgc aaagtaaaaa cactacctct	540
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